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OM nucleic - nucleic search, using sw model

Run on: April 19, 2002, 15:49:05 ; Search time 5842.2 Seconds

(without alignments)
11840.1/6 Million cell updates/sec

Title: US-09-731-457b-3

Perfect score: 4193
Sequence: 1 gtagagcttcgcgcgcgcgt.....agtttaccataaagtag 4193

Scoring table: OLIGO_NDC
Gapco 60.0 , Gapext 60.0

Searched: 1472140 segs, 8248589755 residues

Word size : 0

Total number of hits satisfying chosen parameters: 541028

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
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16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_om:*
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25: em_ro:*
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33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rod:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	28	0.7	39	6	I31174	I31174 Sequence 86
C 2	27	0.6	45	6	I31245	I31245 Sequence 15
C 3	24	0.6	40	6	I31240	I31240 Sequence 15
C 4	23	0.5	50	6	I31257	I31257 Sequence 16
C 5	21	0.5	24	6	AX117030	AX117030 Sequence 16
C 6	21	0.5	40	6	I31263	I31263 Sequence 17
C 7	20	0.5	40	6	AR067269	AR067269 Sequence
C 8	20	0.5	20	6	AR067270	AR067270 Sequence
C 9	20	0.5	21	6	I30547	I30547 Sequence 10
C 10	19	0.5	46	6	I31159	I31159 Sequence 71
C 11	18	0.4	30	6	E32218	E32218 Method for
C 12	18	0.4	43	6	I31458	E32223 Sequence 37
C 13	18	0.4	44	6	E32223	E32223 Method for
C 14	18	0.4	50	6	AX164951	AX164951 Sequence
C 15	18	0.4	50	6	AX164952	AX164952 Sequence
C 16	18	0.4	50	10	MMVIMV21	X89138 M.musculus
C 17	17	0.4	38	6	E32209	E32209 Method for
C 18	17	0.4	42	6	I31141	I31141 Sequence 53
C 19	17	0.4	46	9	CEBSAT3	M19457 C.apella sa
C 20	17	0.4	50	6	AX158289	AX158289 Sequence
C 21	17	0.4	50	9	CEBSAT2	M19456 C.apella sa
C 22	16	0.4	19	6	A91642	A91642 Sequence 16
C 23	16	0.4	19	6	AR074777	AR074777 Sequence
C 24	16	0.4	20	6	AR074792	AR074792 Sequence
C 25	16	0.4	20	6	E05237	E05237 Part of DNA
C 26	16	0.4	24	6	E32214	E32214 Method for
C 27	16	0.4	39	6	I31419	I31419 Sequence 33
C 28	16	0.4	42	6	AR031987	AR031987 Sequence
C 29	16	0.4	42	6	I31431	I31431 Sequence 34
C 30	16	0.4	47	6	I31546	I31546 Sequence 45
C 31	16	0.4	50	6	AX160086	AX160086 Sequence
C 32	15	0.4	15	6	AX11104	AX11104 Oligonucleo
C 33	15	0.4	20	6	AR031002	AR031002 Sequence
C 34	15	0.4	20	6	AR071103	AR071103 Sequence
C 35	15	0.4	20	6	AR074771	AR074771 Sequence
C 36	15	0.4	20	6	AR074776	AR074776 Sequence
C 37	15	0.4	20	6	AR074785	AR074785 Sequence
C 38	15	0.4	20	6	AR121071	AR121071 Sequence
C 39	15	0.4	20	6	E32215	E32215 Method for
C 40	15	0.4	22	6	AR074775	AR074775 Sequence
C 41	15	0.4	22	6	AR074791	AR074791 Sequence
C 42	15	0.4	23	6	AX115975	AX115975 Sequence
C 43	15	0.4	25	6	AX117828	AX117828 Sequence
C 44	15	0.4	25	6	AX117832	AX117832 Sequence
C 45	15	0.4	25	6	AX117836	AX117836 Sequence

ALIGNMENTS

RESULT 1
LOCUS I31174/c 39 bp DNA
DEFINITION Sequence 86 from patent US 5582979.
ACCESSION I31174
VERSION I31174.1 GI:1821965
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 39)
AUTHORS Weber, J.L.
TITLE Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same
JOURNAL Patent: US 5582979-A 86 10-DEC-1996;
FEATURES Location/Qualifiers
source 1..39
/organism="unknown"
BASE COUNT 20 a 18 c 0 g 1 t
ORIGIN

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Query Match      0.7%  Score 28;  DB 6;  Length 39;
Best Local Similarity 100.0%  Pred. No. 0.0011;
Matches 28;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

OY  3849  gtatctgtgtctgtatctgtgtgtctgtc 3876
      |||||
Db   36  gtctgtctgtctgtatctgtctgtctgtc 9

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RESULT	2
LOCUS	I131245/c
DEFINITION	I131245 45 bp DNA
ACCESSION	Sequence 157 from patent US 5582979.
VERSION	I131245
KEYWORDS	I131245.1 GI:1822036
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 45)
TITLE	Weber, J. L.
JOURNAL	Length polymorphisms in (dc-da).sub.n.(dc-dt).sub.n sequences and
FEATURES	Patent: US 5582979-A 157 10-DEC-1996;
source	Location/Qualifiers
	1..45
	/organism="unknown"
BASE COUNT	23 a 21 c 0 g 1 t
ORIGIN	

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Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches    27; Conservative   0; Mismatches     0; Indels     0; Gaps     0;
OY  3850 tttgtgtgtgtgtatgttgtgtgtgtc 3876
Db   |||||||
    45 tctgtgtgtgttctgctgtgtgtgtgtc 19

```

RESULT	3			
LOCUS	131240/c			
DEFINITION	131240	40 bp	DNA	PAT
ACCESSION	Sequence 152	from patent	US 5582979.	06-FEB-1997
VERSION	131240			
KEYWORDS	131240.1	GI:1822031		
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	Unclassified.			
AUTHORS	1 (bases 1 to 40)			
TITLE	Weber, J. L.			
JOURNAL	Length polymorphisms in (dc-da).sub.n.(dc-df).sub.n			
FEATURES	method of using the same			
	Patent: US 5582979-A 152 10-DEC-1996;			
	Location/Qualifiers			
source	1..40			
	/organism="unknown"			
BASE COUNT	20 a	19 c	0 g	1 t
ORIGIN				

	Query Match	0.68;	Score 24;	DB 6;	Length 40;
	Best Local Similarity	100.0%;	Pred. No. 0 21;		
	Matches 24; Conservative	0;	Mismatches	0;	Indels
OY	3849	gtctgctgctgctgcatactgctgtc	3872		Gaps
Dd	24	gtgtgtgtgtgtgtatgtgtgtgt	1		

[illegible]

	Query Match	0.5%	Score 23;	DB 6;	Length 50;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 23; Conservative	0;	Mismatches	0;	Gaps 0;
OY	3853 gtagtgatgtagtggtagtg	3875			
		:			
Db	.50 GGTGCTGGTATAGTGCTGGTC	28			

FEATURES	source
LOCUS	AX117030
DEFINITION	Sequence 2153 from Patent WO0129262.
ACCESSION	AX117030
VERSION	AX117030.1 GI:14033972
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
1 (bases 1 to 24)	
1. Picoult-Newburg, J., and Pohl, M.	
Genotyping reagents, kits and methods of use thereof	
Patent: WO 0129262-A 2153 26-APR-2001;	
Orchid Biosciences, Inc. (US)	
Location/Qualifiers	
1..24	

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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"

BASE COUNT      1 a      0 c      11 g      12 t
ORIGIN

Query Match      0.5%; Score 21; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3854 tggtgtgcatgctgtgtgtc 3874
      |||
Db 1 TGTGTGTGTATGTGTGTGTGT 21

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RESULT	6		PAT	06-FEB-1997
I31263/C				
LOCUS	I31263	40 bp	DNA-	
DEFINITION	Sequence 175 from patent US 5582979.			
ACCESSION	I31263			
VERSION	I31263.1	GI:1822054		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			

Unclassified.
REFERENCE 1 (bases 1 to 40)

AUTHORS Weber J.L.
TITLE Length polymorphisms in (dc-da).sub.n.(dg-dt).sub.n sequences and
method of using the same.

JOURNAL Patent: US 5582979-A 1/5 10-DEC-1996;
FEATURES Location/Qualifiers
source 1..40

BASE COUNT 20 a 19 c 0 g 1 t
ORIGIN

Query Match 0.5%; Score 21; DB 6; Length 40;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3856 tctgtatgtgtgtgtgtgt 3876
|||||

Db 40 TGTGTATGTGTGTGTGTGT 20

RESULT 7
AR067269/c AR067269 20 bp DNA PAT 29-SEP-1999
LOCUS Sequence 617 from patent US 5851760.
DEFINITION AR067269
ACCESSION AR067269
VERSION AR067269.1 GI:5998491
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 20)

AUTHORS Evans G.A. and Smith M.W.
TITLE Method for generation of sequence sampled maps of complex genomes
JOURNAL Patent: US 5851760-A 6/17 22-DEC-1998;
FEATURES Location/Qualifiers
source 1..20

BASE COUNT 5 a 3 c 6 g 6 t
ORIGIN

Query Match 0.5%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4119 caaactgcctcttcgga 4138
|||||

Db 20 CAAACTGCCTCTTCGAAA 1

RESULT 8
AR067270 AR067270 20 bp DNA PAT 29-SEP-1999
LOCUS Sequence 618 from patent US 5851760.
DEFINITION AR067270
ACCESSION AR067270
VERSION AR067270.1 GI:5998492
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Evans G.A. and Smith M.W.
TITLE Method for generation of sequence sampled maps of complex genomes
JOURNAL Patent: US 5851760-A 6/18 22-DEC-1998;
FEATURES Location/Qualifiers
source 1..20

BASE COUNT 5 a 6 c 5 g 4 t
ORIGIN

Query Match 0.5%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4024 atcagctagagcctgact 4043
|||||

Db 1 ATCAGCTAGAGCCTGACT 20

RESULT 9
I30547/c I30547 21 bp DNA PAT 06-FEB-1997
LOCUS Sequence 10 from patent US 5580969.
DEFINITION I30547
ACCESSION I30547
VERSION I30547.1 GI:1821338
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Hoke G.D., Bradley M.O., Williams T.J. and Lee C.
TITLE Antisense oligonucleotides directed against human ICAM-1 RNA
JOURNAL Patent: US 5580969-A 10/03-DEC-1996;
FEATURES Location/Qualifiers
source 1..21

BASE COUNT 11 a 9 c 0 g 1 t
ORIGIN

Query Match 0.5%; Score 20; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3849 gtgtgtgtgtgtgtgtgt 3868
|||||

Db 20 GTGTGTGTGTGTGTGTGT 1

RESULT 10
I31159/c I31159 46 bp DNA PAT 06-FEB-1997
LOCUS Sequence 71 from patent US 5582979.
DEFINITION I31159
ACCESSION I31159
VERSION I31159.1 GI:1821950
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 46)
AUTHORS Weber J.L.
TITLE Length polymorphisms in (dc-da).sub.n.(dg-dt).sub.n sequences and
method of using the same
JOURNAL Patent: US 5582979-A 7/1 10-DEC-1996;
FEATURES Location/Qualifiers
source 1..46

BASE COUNT 23 a 22 c 0 g 1 t
ORIGIN

Query Match 0.5%; Score 19; DB 6; Length 46;
Best Local Similarity 100.0%; Pred. No. 1,6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3858 tctgtatgtgtgtgtgtgt 3876
|||||

Db 46 TGTGTATGTGTGTGTGTGT 28

RESULT 11
E32218/c E32218 30 bp DNA PAT 07-FEB-2001
LOCUS

DEFINITION Method for isolating satellite sequence.
 ACCESSION E32218
 VERSION E32218.1 GI:13021838
 KEYWORDS JP 2000060559-A/20.
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 30)
 AUTHORS Hideaki,T.M.S.S.
 TITLE Method for isolating satellite sequence
 JOURNAL Patent: JP 2000060559-A 20 29-FEB-2000;
 NATL INST OF AGROBIOLOGICAL RESOURCES
 COMMENT OS Halictis discus discus
 PN JP 2000060559-A/20
 PD 29-FEB-2000
 PF 18-AUG-1998 JP 1998232153
 PR HIDEAKI TAKAHASHI,MASASHI SEKINO
 PI C12N15/09,C12Q1/68,C12N15/00
 PC
 CC
 FH Key
 FT source
 FEATURES Location/Qualifiers
 source 1..30
 /organism="unidentified"
 /db_xref="taxon:32644"
 BASE COUNT 15 a 13 c 0 g 2 t
 ORIGIN

Query Match 0.4%; Score 18; DB 6; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 3849 gtgtgtgtgtgtgtgtgt 3866
 Db 19 GTGTGTGTGTGTGTGTGT 2

RESULT 12
 LOCUS I31458 43 bp DNA PAT 06-FEB-1997
 DEFINITION Sequence 370 from patent US 5582979.
 ACCESSION I31458
 VERSION I31458.1 GI:1822249
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 43)
 AUTHORS Weber,J.L.
 TITLE Length polymorphisms in (dc-da).sub.n.(dc-dt).sub.n sequences and
 JOURNAL Patent: US 5582979-A 370 10-DEC-1996;
 FEATURES Location/Qualifiers
 source 1..43
 /organism="unknown"
 BASE COUNT 21 a 19 c 2 g 1 t
 ORIGIN

Query Match 0.4%; Score 18; DB 6; Length 43;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 3849 gtgtgtgtgtgtgtgtgt 3866
 Db 24 GTGTGTGTGTGTGTGTGT 7

RESULT 13
 E32223/c

LOCUS E32223 44 bp DNA PAT 07-FEB-2001
 DEFINITION Method for isolating satellite sequence.
 ACCESSION E32223
 VERSION E32223.1 GI:13021851
 KEYWORDS JP 2000060559-A/25.
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 44)
 AUTHORS Hideaki,T.M.S.S.
 TITLE Method for isolating satellite sequence
 JOURNAL Patent: JP 2000060559-A 25 29-FEB-2000;
 NATL INST OF AGROBIOLOGICAL RESOURCES
 COMMENT OS Halictis discus discus
 PN JP 2000060559-A/25
 PD 29-FEB-2000
 PF 18-AUG-1998 JP 1998232153
 PR HIDEAKI TAKAHASHI,MASASHI SEKINO
 PI C12N15/09,C12Q1/68,C12N15/00
 PC
 CC
 FH Key
 FT source
 FEATURES Location/Qualifiers
 source 1..44
 /organism="unidentified"
 /db_xref="taxon:32644"
 BASE COUNT 17 a 20 c 7 g 0 t
 ORIGIN

Query Match 0.4%; Score 18; DB 6; Length 44;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 3845 gtgtgtgtgtgtgtgtgt 3862
 Db 19 GTGTGTGTGTGTGTGTGT 2

RESULT 14
 LOCUS AX164951 50 bp DNA PAT 22-JUN-2001
 DEFINITION Sequence 146 from Patent WO0138586.
 ACCESSION AX164951
 VERSION AX164951.1 GI:14545780
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 50)
 AUTHORS Shinketsu,R.A. and Leach,M.
 TITLE Nucleic acids containing single nucleotide polymorphisms and
 JOURNAL methods of use thereof
 Patent: WO 0138586-A 146 31-MAY-2001;
 Curagen Corporation (US)
 FEATURES Location/Qualifiers
 source 1..50
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 misc_feature 25..26
 /note="Nucleotide deleted between bases 25 and 26
 Accession number cg41653463"
 variation 26
 /note="single nucleotide polymorphism"
 BASE COUNT 1 a 3 c 20 g 26 t
 ORIGIN

Query Match 0.4%; Score 18; DB 6; Length 50;
 Best Local Similarity 100.0%; Pred. No. 5.8e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3845 gtgcgtgtgtgtgtgtgt 3862
|||||
Db 6 GTGCTGTGTGTGTGTGT 23

RESULT 15

AXI64952 50 bp DNA PAT 22-JUN-2001
LOCUS
DEFINITION Sequence 147 from Patent WO0138586.
ACCESSION AXI64952
VERSION AXI64952.1 GI:14545781
KEYWORDS

SOURCE

ORGANISM human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 50)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and
methods of use thereof
JOURNAL Patent: WO 0138586-A 147 31-MAY-2001;
Curagen Corporation (US)
FEATURES
Source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
misc_feature 25..26
/note="Nucleotide deleted between bases 25 and 26
Accession number cg41653463"
variation 26
/note="single nucleotide polymorphism"
BASE COUNT 1 a 3 c 21 g 25 t
ORIGIN

Query Match 0.4%; Score 18; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3845 gtgcgtgtgtgtgtgtgt 3862
|||||
Db 5 GTGCTGTGTGTGTGTGT 22

RESULT 16

MVIMV21 50 bp DNA ROD 30-AUG-1996
LOCUS
DEFINITION M.musculus DNA for vimentin-binding fragment V21.
ACCESSION X89138
VERSION X89138.1 GI:887544
KEYWORDS
SOURCE
ORGANISM Mus musculus
house mouse.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 50)
AUTHORS Wang, X., Tolstosov, G., Shoeman, R.L. and Tryub, P.
TITLE Selective binding of specific mouse genomic DNA fragments by mouse
vimentin filaments in vitro
JOURNAL DNA Cell Biol. 15 (3), 209-225 (1996)
MEDLINE 96226400
REFERENCE 2 (bases 1 to 50)
AUTHORS Shoeman, R.L.
TITLE Direct Submission
JOURNAL Submitted (23-JUN-1995) Shoeman R. L., Max-Planck-Institute fuer
zeilbiologie, Rosenhof, Ladenburg, Germany, D-68526
COMMENT On Jul 6, 1995 this sequence version replaced g1:872146.
FEATURES
Source Location/Qualifiers
1..50
/organism="Mus musculus"
/db_xref="taxon:10090"

protein_bind

/cell_line="Ehrlich ascites tumor cell"
1..50
/standard_name="fragment V21 in citation #1"
/citation-[1]
/bound_moiety="vimentin"
/function="sequence bound by vimentin filaments in vitro"
/evidence="experimental"
3..50
repeat_region
/partial
/citation-[1]
/rpt_family="d(CA/GT)n dinucleotide repeats, imperfect"
/rpt_unit=3..4
/function="recombination, potentially to form non-B DNA"
/evidence="experimental"
/rpt_type=DIRECT

BASE COUNT 3 a 2 c 19 g 26 t
ORIGIN

Query Match 0.4%; Score 18; DB 10; Length 50;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3849 gtgtgtgtgtgtgtgtgt 3866
|||||
Db 3 GTGCTGTGTGTGTGTGT 20

RESULT 17

E32209/c 38 bp DNA PAT 07-FEB-2001
LOCUS
DEFINITION Method for isolating satellite sequence.
ACCESSION E32209
VERSION E32209.1 GI:13021808
KEYWORDS JP 2000060559-A/11.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 38)
AUTHORS Hideaki, T.M.S.S.
TITLE Method for isolating satellite sequence
JOURNAL Patent: JP 2000060559-A 11 29-FEB-2000;
NATL INST OF AGRICULTURAL RESOURCES
COMMENT OS Haliotis discus discus
PN JP 2000060559-A/11
PD 29-FEB-2000
PF 18-AUG-1998 JP 1998232153
PR
PI HIDEAKI TAKAHASHI, MASASHI SEKINO
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CC
FH
FT Key Location/Qualifiers
FT source 1..38
/organism="Haliotis discus discus",
Location/Qualifiers
1..38
/db_xref="taxon:32644"

BASE COUNT 18 a 18 c 0 g 2 t
ORIGIN

Query Match 0.4%; Score 17; DB 6; Length 38;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3860 tgtatgtgtgtgtgtgtgt 3876
|||||
Db 38 TGTATGTGTGTGTGTGTGT 22

RESULT 18
I31141/c 42 bp DNA PAT 06-FEB-1997
LOCUS I31141

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DEFINITION      Sequence 53 from patent US 5582979.
ACCESSION       I31141
VERSION         I31141.1 GI:1821932
KEYWORDS
SOURCE          Unknown.
ORGANISM        Unknown.
REFERENCE       1 (bases 1 to 42)
AUTHORS         Weber, J.L.
TITLE           Length polymorphisms in (dc-da).sub.n.(dc-dt).sub.n sequences and
                method of using the same
JOURNAL         Patent: US 5582979-A 53 10-DEC-1996;
FEATURES        Location/Qualifiers
                source          1..42
                /organism="unknown"
BASE COUNT      21 a 20 c 0 g 1 t
ORIGIN
Query Match     0.4%; Score 17; DB 6; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3849 gtcgtgtgtgtgtgtgtgt 3865
Db 17 GTCTGTGTGTGTGTGTATG 1

RESULT 19
CEBSAT3         46 bp  DNA
LOCUS           C.apella satellite DNA, clone pCP3.
DEFINITION     M19457 J03907
ACCESSION      M19457.1 GI:176633
VERSION        M19457.1 GI:176633
KEYWORDS       repeat region; satellite repeat.
SOURCE         C.apella DNA, clone pCP3.
ORGANISM       Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus.
REFERENCE       1 (bases 1 to 46)
AUTHORS         Vogt, N., Rousseau, N., Leng, M. and Malfoy, B.
TITLE           A study of the B-2 transition of the AC-rich region of the repeat
                unit of a satellite DNA from Cebus by means of chemical probes
JOURNAL         J. Biol. Chem. 263, 11826-11832 (1988)
MEDLINE        88298859
COMMENT        Draft entry and computer-readable sequence for [1] kindly provided
                by B.Malfoy, 15-JUN-1988.
FEATURES        Location/Qualifiers
                source          1..46
                /organism="Cebus apella"
                /db_xref="taxon:9515"
BASE COUNT      3 a 4 c 19 g 20 t
ORIGIN          Unreported.
Query Match     0.4%; Score 17; DB 9; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3846 tgcgtgtgtgtgtgtgtgt 3862
Db 6 TCGGTGTGTGTGTGTGTGT 22

RESULT 20
AX158289        50 bp  DNA
LOCUS           AX158289
DEFINITION     Sequence 1617 from Patent WO0140521.
ACCESSION      AX158289
VERSION        AX158289.1 GI:14539620
KEYWORDS
SOURCE         human.
ORGANISM       Homo sapiens

```

```

Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE       1 (bases 1 to 50)
AUTHORS         Shinkets, R.A. and LeGsch, M.
TITLE           Nucleic acids containing single nucleotide polymorphisms and
                methods of use thereof
JOURNAL         Patent: WO 0140521-A 1617 07-JUN-2001;
                Curagen Corporation (US)
FEATURES        Location/Qualifiers
                source          1..50
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                misc_feature     25..26
                /note="Nucleotide deleted between bases 25 and 26
                Accession number cg32149517"
                misc_feature     26
                /note="1 of 2 allelic variants (1618 is other entry)"
BASE COUNT      3 a 7 c 20 g 20 t
ORIGIN
Query Match     0.4%; Score 17; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3855 gtcgtgtgtgtgtgtgtgt 3871
Db 34 GTGTGTGTGTGTGTGTGTG 50

RESULT 21
CEBSAT2         50 bp  DNA
LOCUS           C.apella satellite DNA, clone pCP2.
DEFINITION     M19456 J03907
ACCESSION      M19456.1 GI:176632
VERSION        M19456.1 GI:176632
KEYWORDS       repeat region; satellite repeat.
SOURCE         C.apella DNA, clone pCP2.
ORGANISM       Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Cebus.
REFERENCE       1 (bases 1 to 50)
AUTHORS         Vogt, N., Rousseau, N., Leng, M. and Malfoy, B.
TITLE           A study of the B-2 transition of the AC-rich region of the repeat
                unit of a satellite DNA from Cebus by means of chemical probes
JOURNAL         J. Biol. Chem. 263, 11826-11832 (1988)
MEDLINE        88298859
COMMENT        Draft entry and computer-readable sequence for [1] kindly provided
                by B.Malfoy, 15-JUN-1988.
FEATURES        Location/Qualifiers
                source          1..50
                /organism="Cebus apella"
                /db_xref="taxon:9515"
BASE COUNT      2 a 4 c 20 g 24 t
ORIGIN          Unreported.
Query Match     0.4%; Score 17; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3846 tgcgtgtgtgtgtgtgtgt 3862
Db 6 TCGGTGTGTGTGTGTGTGT 22

RESULT 22
A91642/c        19 bp  DNA
LOCUS           A91642
DEFINITION     Sequence 169 from Patent WO9824928.
ACCESSION      A91642
VERSION        A91642.1 GI:6740597
KEYWORDS

```


SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 19)
AUTHORS Pallisgaard, N. and Hokland, P.
TITLE DETECTION OF CHROMOSOMAL ABNORMALITIES
JOURNAL Patent: WO 9824928-A 169 11-JUN-1998;
PALLISGAARD NIELS (DK); HOKLAND PETER (DK)
FEATURES
source 1..19
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 4 a 7 c 3 g 5 t
ORIGIN

Query Match 0.4%; Score 16; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1701 tggacatgaagtcgc 1716
Db 19 TGGACATGAGTGC 4

RESULT 23
LOCUS AR074777 19 bp DNA PAT 28-AUG-2000
DEFINITION Sequence 74 from patent US 5955276.
ACCESSION AR074777
VERSION AR074777.1 GI:10001530
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 19)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic polymorphisms
JOURNAL Patent: US 5955276-A 74 21-SEP-1999;
FEATURES
source 1..19
Location/Qualifiers
BASE COUNT 2 a 0 c 7 g 10 t
ORIGIN

Query Match 0.4%; Score 16; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3849 gtgtgtgtgtgtat 3864
Db 2 GTGTGTGTGTGTAT 17

RESULT 24
LOCUS AR074792 20 bp DNA PAT 28-AUG-2000
DEFINITION Sequence 89 from patent US 5955276.
ACCESSION AR074792
VERSION AR074792.1 GI:10001545
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 20)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic polymorphisms
JOURNAL Patent: US 5955276-A 89 21-SEP-1999;
FEATURES
source 1..20
Location/Qualifiers

BASE COUNT 10 a 7 c 0 g 3 t
ORIGIN

Query Match 0.4%; Score 16; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3849 gtgtgtgtgtgtat 3864
Db 19 GTGTGTGTGTGTAT 4

RESULT 25
LOCUS E05237/c 20 bp DNA PAT 29-SEP-1997
DEFINITION Part of DNA sequence of Human papillomavirus 11.
ACCESSION E05237
VERSION E05237.1 GI:2173427
KEYWORDS JP 1993192200-A/7.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 20)
AUTHORS Okazawa, K., Shimada, M., Katou, I., Fukushima, M. and Fujinaga, K.
TITLE DETECTION OF HUMAN PAPILLOMA VIRUS
JOURNAL Patent: JP 1993192200-A 7 03-AUG-1993;
TAKARA SHUZO CO LTD
COMMENT OS Artificial gene
OC Artificial sequence; Genes.
OS Human papillomavirus
PN JP 1993152200-A/7
PD 03-AUG-1993 JP 1991230839
PF 19-AUG-1991 JP 1991230839
PR 20-AUG-1990 JP 90P 217067
PI OKAZAWA KAZUHIDE, SHIMADA MASAMITSU, KATOU IKUNOSHIN, PI
FUKUSHIMA MICHIO,
FUJINAGA KEI
PC C1201/70.C1201/68;
CC strandedness: Single;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FEATURES
source 1..20
Location/Qualifiers
BASE COUNT 6 a 6 c 3 g 5 t
ORIGIN

Query Match 0.4%; Score 16; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2382 tgtcagcagtgtaag 2397
Db 16 TGTCCAGCAGTGAAG 1

RESULT 26
LOCUS E32214/c 24 bp DNA PAT 07-FEB-2001
DEFINITION Method for isolating satellite sequence.
ACCESSION E32214
VERSION E32214.1 GI:13021823
KEYWORDS JP 2000060559-A/16.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 24)
AUTHORS HIDEAKI, T.M.S.S.

TITLE	Method for isolating satellite sequence
JOURNAL	Patent: JP 2000060559-A 16 29-FEB-2000;
COMMENT	NATL INST OF AGROBIOLOGICAL RESOURCES
	OS Halolitis discus discus
	PN TD 2000060559.2/16

PF 18-AUG-1998 JP 1998232153
PR

PI HIDEAKI TAKAHASHI, MASASHI SEKINO
PC C12N15/09, C12Q1/68, C12N15/00

Key	Location/Qualifiers
FH	1. .24
FT	/organism='Haliotis
FT	

FEATURES	location/Qualifiers
source	1..24
	/organism="unidentified"
	/db_xref="taxon:32644"
BASE COUNT	8 a 12 c 4 g 0 t
ORIGIN	

Query Match	0.4%	Score 16	DB 6	Length 24
Best Local Similarity	100.0%	Pred. No.	8	1e+03
Matches 16	Conservative 0	Mismatches 0	Indels 0	Gaps 0

```
QY      3847  gcgtgctgtgtgtgt 3862
          |||||
Db      19  GCGTGTGTGTGT 4
```

RESULT 27			
I31419/c			
LOCUS	I31419	39 bp	DNA
DEFINITION:	Sequence 331	from patent US 5582979.	PAT
			06-FEB-1997

ACCESSION	131419
VERSION	131419.1
KEYWORDS	GI:1822210
SOURCE	Unknown.
ORGANISM	Unknown.

REFERENCE	Unclassified.
1 (Bases 1 to 39)	
AUTHORS	Weber, J. L.
TITLE	Length Polymorphisms in (dc-da).sub.n.(dc-dt).sub.n sequences and method of using the same
JOURNAL	Patent: US 5582979-A 331 10-DEC-1996;
FEATURES	Location/Qualifiers
SOURCE	1. .39

/organism-unknown-			
BASE COUNT	19 a	14 c	0 g
ORIGIN			6 t

Query Match	0.4%	Score 16	DB 6	Length 39
Best Local Similarity	100.0%	Pred. No.	8.1e+03	
Match 16, Conservative	0	Mismatches	0	Gaps 0

QY	3849	gtgtgtgtgtgtgtat	3864
Db	24	GTGTGTGTGTGTAT	9

RESULT 28		29-SEP-1996	
AR031987/c			
LOCUS	AR031987	42 bp	DNA
DEFINITION	Sequence 10 from patent US 5866553.		
ACCESSION	AR031987		
VERSION	AR031987.1	GI:5946276	

SOURCE	ORGANISM	REFERENCE
Unknown.	Unknown.	1 (bases 1 to 42)
Unclassified.		

```

AUTHORS  Donnelly,J.J., Liu,M.A., Martner,D. and Montgomery,D.L
TITLE    Polynucleotide vaccine for papillomavirus
JOURNAL  Patent: US 5866553-A 10 02-FEB-1999;
FEATURES Location/Qualifiers
          1. .42
BASE COUNT      19 a      13 c      2 g      8 t
ORIGIN

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Query Match	0.4%	Score 16;	DB 6;	Length 42;
Best Local Similarity	100.0%;	Pred. No. 8.1e+03;		
Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	215	ttagagatctatgtg	230
Db	16	TTAGAGATCTATGTG	1

	RESULT	29	
I31A31/c.			
LOCUS	I31A31	42 bp	DNA
DEFINITION	Sequence 343 from patent US 5582979.		PAT
FEATURES			
			06-FEB-1997

SOURCE ORGANISM	REFERENCE
Unknown.	1 (bases 1 to 42)
Unknown.	1 (bases 1 to 42)
Unclassified.	1 (bases 1 to 42)

FEATURES	source
JOURNAL	1
TITLE	42
AUTHORS	
WEAVER, J. A.	
Length polymorphisms in (dc-da), sub. n. (dc-dt), sub. n sequences and	
method of using the same	
Patent: US 5582979-A 343 10-DEC-1996;	
Location/Qualifiers	

SOURCE	/organism="unknown"	
BASE COUNT	19 a	17 c
ORIGIN	3 g	3 t

Query Match	0.48;	Score 16;	DB 6;	Length 42;
Best Local Similarity	100.08;	Pred. No. 8.1e+03;		
Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

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QY      3849  gtgtgtgtgtgtgtat 3864
          |||||
Db      24  GTGTGTGTGTGTAT 9

```

LOCUS	DEFINITION	SEQUENCE	LOCUS	DEFINITION	SEQUENCE
131546/c	Sequence 458 from patent US 5582979.	131546	131546/c	Sequence 458 from patent US 5582979.	131546

SOURCE	ORGANISM	REFERENCE
Unknown.	Unknown.	1 (bases 1 to 47
Unknown.	Unclassified.	

AVTIONS	newer, U.S.
TITLE	Length polymorphisms in (dc-da), sub.n. (dg-dt), sub.n sequences and
JOURNAL	method of using the same
FEATURES	Patent: US 5582979-A 458 10-DEC-1996;
	Location/Qualifiers

source	1. 47	
BASE COUNT	23 a	22 c 1 g
ORIGIN		

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query match      0.48;  Score 16;  DB 6;  Length 47;
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Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3861 gtatgtgtgtgtgtgt 3876
DB 34 GTATGTGTGTGTGT 19

RESULT 31
AX160086/c AX160086 50 bp DNA PAT 22-JUN-2001
LOCUS Sequence 3414 from Patent WO0140521.
DEFINITION AX160086
ACCESSION AX160086
VERSION AX160086.1 GI:14541417
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 50)
AUTHORS Shimkets, R.A. and Leach, M.
TITLE Nucleic acids containing single nucleotide polymorphisms and methods of use thereof
JOURNAL Patent: WO 0140521-A 3414 07-JUN-2001;
Curagen Corporation (US)
LOCATION/Qualifiers

FEATURES
source 1..50
misc_feature /db_xref="taxon:9606"
25..26
/note="Nucleotide deleted between bases 25 and 26
Accession number cg43267337"

misc_feature 26
/note="2 of 2 allelic variants (3413 is other entry)"
BASE COUNT 32 a 11 c 3 g 4 t
ORIGIN

Query Match 0.4%; Score 16; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3849 gtgtgtgtgtgtgtat 3864
DB 16 GTGTGTGTGTGTAT 1

RESULT 32
A11104/c A11104 15 bp DNA PAT 03-DEC-1993
LOCUS
DEFINITION Oligonucleotide L3.
ACCESSION A11104
VERSION A11104.1 GI:490954
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.

REFERENCE 1 (bases 1 to 15)
AUTHORS Ikebara, M. and Kida, M.
TITLE Synthetic gene for human lysozyme
JOURNAL Patent: EP 0181634-A 48 21-MAY-1986;
Takeda Chemical Industries, Ltd
LOCATION/Qualifiers

FEATURES
source 1..15
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 5 a 4 c 1 g 5 t
ORIGIN

Query Match 0.4%; Score 15; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2922 accttgagagatg 2936
DB 15 ACCTTGAGAGATTG 1

RESULT 33
AR031002 AR031002 20 bp DNA PAT 29-SEP-1999
LOCUS Sequence 13 from patent US 5861502.
DEFINITION AR031002
ACCESSION AR031002
VERSION AR031002.1 GI:5944216
KEYWORDS
SOURCE unknown.
ORGANISM unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Prockop, D., Collige, A., Baserga, R. and Nugent, P.
TITLE Antisense oligonucleotides to inhibit expression of mutated and wild type genes for collagen
JOURNAL Patent: US 5861502-A 13 19-JAN-1999;
LOCATION/Qualifiers

FEATURES
source 1..20
BASE COUNT 2 a 6 c 5 g 7 t
ORIGIN

Query Match 0.4%; Score 15; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3599 gtctctgagcatg 3613
DB 4 GTCTCTGAGCATG 18

RESULT 34
AR071103/c AR071103 20 bp DNA PAT 18-FEB-2000
LOCUS Sequence 1 from patent US 5910410.
DEFINITION AR071103
ACCESSION AR071103.1 GI:7221991
VERSION
KEYWORDS
SOURCE unknown.
ORGANISM unknown.

REFERENCE 1 (bases 1 to 20)
AUTHORS Lichtenwalter, K. and Ward, C.B.
TITLE Dual tag binding assay
JOURNAL Patent: US 5910410-A 1 08-JUN-1999;
LOCATION/Qualifiers

FEATURES
source 1..20
/organism="unknown"
BASE COUNT 2 a 10 c 3 g 5 t
ORIGIN

Query Match 0.4%; Score 15; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1193 gtgacctgagagag 1207
DB 19 GTGACCTGAGAGG 5

RESULT 35
AR074771 AR074771 20 bp DNA PAT 28-AUG-2000
LOCUS Sequence 68 from patent US 5955276.
DEFINITION AR074771
ACCESSION AR074771.1 GI:10001524
VERSION

KEYWORDS
SOURCE Unknown.
ORGANISM Unidentified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic polymorphisms
JOURNAL Patent: US 5955276-A 68 21-SEP-1999;
FEATURES Location/Qualifiers
source 1..20
BASE COUNT 3 a 0 c 7 g 10 t
ORIGIN

Query Match 0.4%; Score 15; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3862 tatgtgtgtgtgt 3876
|||||
Db 5 TATGTGTGTGTGT 19

RESULT 36
AR074776 20 bp DNA PAT 28-AUG-2000
LOCUS AR074776/c
DEFINITION Sequence 73 from patent US 5955276.
ACCESSION AR074776
VERSION AR074776.1 GI:10001529
KEYWORDS
SOURCE Unknown.
ORGANISM Unidentified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic polymorphisms
JOURNAL Patent: US 5955276-A 73 21-SEP-1999;
FEATURES Location/Qualifiers
source 1..20
BASE COUNT 10 a 7 c 0 g 3 t
ORIGIN

Query Match 0.4%; Score 15; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3862 tatgtgtgtgtgt 3876
|||||
Db 17 TATGTGTGTGTGT 3

RESULT 37
AR074785 20 bp DNA PAT 28-AUG-2000
LOCUS AR074785
DEFINITION Sequence 82 from patent US 5955276.
ACCESSION AR074785
VERSION AR074785.1 GI:10001538
KEYWORDS
SOURCE Unknown.
ORGANISM Unidentified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Morgante, M. and Vogel, J. Marie.
TITLE Compound microsatellite primers for the detection of genetic polymorphisms
JOURNAL Patent: US 5955276-A 82 21-SEP-1999;
FEATURES Location/Qualifiers
source 1..20

BASE COUNT 3 a 0 c 7 g 10 t
ORIGIN

Query Match 0.4%; Score 15; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3862 tatgtgtgtgtgt 3876
|||||
Db 5 TATGTGTGTGTGT 19

RESULT 38
AR121071 20 bp DNA PAT 16-MAY-2001
LOCUS AR121071/c
DEFINITION Sequence 92 from patent US 6159694.
ACCESSION AR121071
VERSION AR121071.1 GI:14104647
KEYWORDS
SOURCE Unknown.
ORGANISM Unidentified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Karris, J. G.
TITLE Antisense modulation of stat3 expression
JOURNAL Patent: US 6159694-A 92 12-DEC-2000;
FEATURES Location/Qualifiers
source 1..20
BASE COUNT 4 a 4 c 6 g 6 t
ORIGIN

Query Match 0.4%; Score 15; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2837 tacctgaagaccag 2851
|||||
Db 17 TACCTGAAGACCAAG 3

RESULT 39
E32215 20 bp DNA PAT 07-FEB-2001
LOCUS E32215/c
DEFINITION Method for isolating satellite sequence.
ACCESSION E32215
VERSION E32215.1 GI:13021826
KEYWORDS JP 2000060539-A/17.
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 20)
AUTHORS Hideaki, T. M. S. S.
TITLE Method for isolating satellite sequence
JOURNAL Patent: JP 2000060539-A 17 29-FEB-2000;
COMMENT NATL INST OF AGRICULTURAL RESOURCES
OS Haliotis discus discus
PN JP 2000060539-A/17
PD 29-FEB-2000
PF 18-AUG-1998 JP 1998232153
PR
PI HIDEAKI TAKAHASHI, MASASHI SEKINO
PC C12N15/09, C12Q1/68, C12N15/00
CC
FH key Location/Qualifiers
FT source 1..20
FEATURES Location/Qualifiers
source 1..20
/organism="undidentified"

BASE COUNT 6 a /db_xref="taxon:32644" 0 t
ORIGIN 10 c 4 g

Query Match 0.4%; Score 15; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3847 gctgtgtgtgtgtgt 3861
|||||
Db 15 GCGTGTGTGTGTGTG 1

RESULT 40
AR074775/c AR074775 22 bp DNA PAT 28-AUG-2000
LOCUS AR074775
DEFINITION Sequence 72 from patent US 5955276.
ACCESSION AR074775
VERSION AR074775.1 GI:10001528
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 22)
AUTHORS Morgante,M. and Vogel,J.Marie.
TITLE Compound microsatellite primers for the detection of genetic polymorphisms
JOURNAL Patent: US 5955276-A 72 21-SEP-1999;
FEATURES Location/Qualifiers
source 1..22
/organism="unknown"

BASE COUNT 11 a 6 c 0 g 5 t
ORIGIN

Query Match 0.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3862 tatgtgtgtgtgtgt 3876
|||||
Db 15 TATGTGTGTGTGTGT 1

RESULT 41
AR074791/c AR074791 22 bp DNA PAT 28-AUG-2000
LOCUS AR074791
DEFINITION Sequence 88 from patent US 5955276.
ACCESSION AR074791
VERSION AR074791.1 GI:10001544
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 22)
AUTHORS Morgante,M. and Vogel,J.Marie.
TITLE Compound microsatellite primers for the detection of genetic polymorphisms
JOURNAL Patent: US 5955276-A 88 21-SEP-1999;
FEATURES Location/Qualifiers
source 1..22
/organism="unknown"

BASE COUNT 11 a 6 c 0 g 5 t
ORIGIN

Query Match 0.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3850 tctgtgtgtgtgtat 3864
|||||

Db 22 TGTGTGTGTGTGTAT 8

RESULT 42

AX115975 AX115975 23 bp DNA PAT 11-MAY-2001
LOCUS AX115975
DEFINITION Sequence 1098 from Patent WO0129262.
ACCESSION AX115975
VERSION AX115975.1 GI:14032917
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.

REFERENCE 1 (bases 1 to 23)
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 1098 26-APR-2001;
FEATURES Location/Qualifiers
source 1..23
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Primer"

BASE COUNT 3 a 4 c 8 g 8 t
ORIGIN

Query Match 0.4%; Score 15; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 3e+04;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3848 cgtgtgtgtgtgtgt 3862
|||||
Db 8 CGTGTGTGTGTGTGT 22

RESULT 43
AX117828/c AX117828 25 bp DNA PAT 11-MAY-2001
LOCUS AX117828
DEFINITION Sequence 2951 from Patent WO0129262.
ACCESSION AX117828
VERSION AX117828.1 GI:14034779
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequence.

REFERENCE 1 (bases 1 to 25)
AUTHORS Picoult-Newburg,L. and Pohl,M.
TITLE Genotyping reagents, kits and methods of use thereof
JOURNAL Patent: WO 0129262-A 2951 26-APR-2001;
FEATURES Location/Qualifiers
source 1..25
/organism="synthetic construct"
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OY 3848 cgtgtgtgtgtgtgt 3862
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RESULT 44
AX117832/c AX117832 25 bp DNA PAT 11-MAY-2001
LOCUS AX117832
DEFINITION Sequence 2955 from Patent WO0129262.

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 VERSION AX117832.1 GI:14034783
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Picoult-Newburg, L. and Pohl, M.
 TITLE Genotyping reagents, kits and methods of use thereof
 JOURNAL Patent: WO 0129262-A 2955 26-APR-2001;
 Orchid Biosciences, Inc. (US)
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RESULT 45
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 DEFINITION Sequence 2959 from Patent WO0129262.
 ACCESSION AX117836
 VERSION AX117836.1 GI:14034787
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Picoult-Newburg, L. and Pohl, M.
 TITLE Genotyping reagents, kits and methods of use thereof
 JOURNAL Patent: WO 0129262-A 2959 26-APR-2001;
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